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| 10/725,906 | 12/01/2003 | Renu Wadhwa | 14875-066002 | 5573 |

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| EXAMINER | |
|---|---|
| BELYAVSKYI, MICHAIL A | |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1644 | |

DATE MAILED: 03/09/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

| Office Action Summary | Application No. | Applicant(s) | |
|---|---|---|---|
| | 10/725,906 | WADHWA ET AL. | |
| | Examiner | Art Unit | |
| | Michail A. Belyavskyi | 1644 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *06 January 2006*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *8-11,13,15,17-20,22-25,28 and 34-50* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☒ Claim(s) *8-10,,17-19,22-24,28,44,46,49 and 50* is/are allowed.

6)☒ Claim(s) *11,15,20,25,34-43,45,47 and 48* is/are rejected.

7)☒ Claim(s) *13* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

RESPONSE TO APPLICANT'S AMENDMENT

1. Applicant's amendment, filed 01/06/06 is acknowledged.

Claims 8-11, 13, 15, 17-20, 22-25, 28 and 34-50 are pending and under consideration in the instant application.

In view of the amendment, filed 01/06/06 the following objection and rejections remain:

2. The specification is objected to under 37 CFR 1.821(d) for failing to disclose SEQ ID NOs, for the amino acid sequence disclosed on page 18, line 2.

Applicant asserts that a sequence identifier for the sequence was added in the amendment dated January 14, 2002.

It is noted however that there are two amendments of record in the instant application: one filed on 12/01/03 and the other one filed on 01/06/06. None of said amendments comprises sequence identifier for the amino acid sequence disclosed on page 18, line 2.

3. The following is a quotation of the first paragraph of 35 U.S.C. 112:

*The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.*

4. Claims 11, 15, 20, 25, 34-43, and 45 stand rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1, or an isolated nucleic acid that encodes a polypeptide **consisting** of the amino acid sequence 76 through 149 of SEQ ID NO:1, or **consisting** of the amino acid sequence 1-75 of SEQ ID NO:1 wherein said polypeptide inhibits the differentiation of myoblasts into myotubes does not reasonably provide enablement for : (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes, as claimed in claim 11, or (ii) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (iii) *any* isolated nucleic acid encoding a polypeptide which

comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (iv) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims 37-39; or (v) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (vi) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (vii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claim 45. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims for the same reasons set forth in the previous Office Action, mailed on 07/07/05

Applicant's arguments, filed 01/06/06 have been fully considered, but have not been found convincing.

Applicant asserts that ; (i) properly interpreted, the sence/antisense aspect of claim 11 does not raise any enablement issues; (ii) the hybridization conditions specified in the claims are high stringency conditions and as such require a high degree of complementarity to the probe in order to produce hybridization; (iii) A working examples of antisense molecule that inhibits the expression of a polypeptide comprising SEQ ID NO: 1 is disclosed in Examples 8 and 9 of the instant specification; (iv) in making the enablement rejection the Examiner ignored the limitation that the encoded polypeptide 'inhibits the differentiation of myoblasts into myotubes"; (v) using the open-ended term "comprising" to permit exactly the expansion of the scope of nucleic acid claims is perfectly acceptable. One skill in the art would easily be able to use standard techniques to append any desired sequence.

Contrary to Applicant's assertion, it is the Examiner position that the Specification disclosed a discovery of a "striamin" polypeptide of SEQ ID NO:1, encoded by an nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said polypeptide inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 ( see entire document, pages 17 and overlapping pages 20-21 and Fig.1 in particular). The Specification explicitly disclosed that **only the full length protein consisting of** amino acid sequences 1-149 of SEQ ID NO:1, encoded by nucleotides 294 through 740 of SEQ ID NO:2; or polypeptide **consisting** of amino acid sequences of residues 76 through 149 of SEQ ID NO:1 can inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 ( see Examples 8- 11 in particular).

Applicant has not taught how to make and/or use : (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into

myotubes, as claimed in claim 11, or (ii) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (iii) *any* isolated nucleic acid encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (iv) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims 37-39; or (v) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (vi) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (vii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claim 45. The structural characteristics of said nucleic acid molecules are not defined in the claims.

With regards to the issue that " properly interpreted, the sence/antisense aspect of claim 11 does not raise any enablement issues".

It is the Examiner position that claim 11 does raise the enablement issue. Claim 11 recites an isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes. The claim as written reads on antisense nucleic acid. The translation of said complementary (antisense) nucleic acid sequence does not encode the "striamin" polypeptide of SEQ ID NO:1.

With regards to the issue that "the hybridization conditions specified in the claims are high stringency conditions and as such require a high degree of complementarity to the probe in order to produce hybridization".

The fact that two nucleic acid sequences will hybridize under stringent conditions does not require that the two sequences are 100% identical, encoded the same polypeptide or share any functional activity. Thus, the same observations apply to the recitation of "isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes. It was well known in the art at the time the invention was made that hybridization could occur between two sequence based upon short stretches of 100% identity. Thus a great deal of sequence variability *with respect to the full-length nucleic acid* is possible and can reads on the nucleic acid having less than 100 % identity over the full length of SEQ ID NO:1. Since the instant specification does not disclosed any essential structural characteristics of nucleic acid molecule of SEQ ID NO:2 that are associated with the function of the encoded "striamin" polypeptide of SEQ ID NO:1 the hybridization language does not allow the skilled artisan to make an nucleic acids commensurate in scope with the instant claims without undue experimentation.

With regards to the comments that a working examples of antisense molecule that inhibits the expression of a polypeptide comprising SEQ ID NO: 1 is disclosed in Examples 8 and 9 of the instant specification.

Contrary to Applicant's assertion, the Examples 8 and 9 of the instant Specification only disclosed that expression of full length striamin-S reduced the p53 activity, compared to the control. There is no teaching that expression of antisense strand *inhibits the expression* of steriamin-S. Said examples only disclosed that in the cells wherein antisense strriamin has been expressed, the activity of p53 slightly increases, compare to the control. However, one skilled in the art would know that said results does not inherently interpreted as inhibition of the expression. The use of antisense nucleic acid to inhibit expression of a polypeptide comprising SEQ ID NO:1as claimed in claim 15 is well known in the art to be highly unpredictable, even though the level of skill in the art is high. For instance, Mountain reviews in TIBTECH (18:119-128 2000) that while much progress has been made in the field of gene therapy, developing effective gene therapies is much more demanding than originally anticipated (e.g., pg 120, middle); and that most of the difficulty lies with the development of effective vectors since the vectors in use all have both advantages and disadvantages (e.g., Table 4). Mountain concludes that it is unlikely that a universal vector will emerge in the next few years (page 125, middle of 1st column). Similarly, although antisense therapy has progressed in recent years, there is still a high level of unpredictability in the art. This unpredictability was summarized recently by Branch (TIBS 1998; 23:45-50). In particular, difficulties in ensuring that the oligo interacts with its single gene target versus other genes, and a variety of unexpected non-antisense effects, complicate the use of antisense compounds (e.g., summarized in Abstract). Thus in the absence of working examples or detailed guidance in the specification, the intended uses of an antisense nucleic acid are fraught with uncertainties.

With regards to the comments that "in making the enablement rejection the Examiner ignored the limitation that the encoded polypeptide 'inhibits the differentiation of myoblasts into myotubes"

It is noted that said limitation only added the function of the polypeptide. However, said limitation does not obviate the issues of enablement rejection set forth in the previous office action of 07/07/05 and has not been ignored. The enablement issues of making the protein still remain because the specification does not teach and provide sufficient guidance as to which amino acid of SEQ ID NO:1 would have been altered such that the resultant polypeptide would have retained the function of a striamin polypeptide of SEQ ID NO:1. Therefore, absent the ability to predict which of these peptides would function as claimed, and given the lack of data on regions critical for activity, for one of skill in the art to practice the invention as claimed would require a level of experimentation that is excessive and undue.

The instant claims encompass in their breadth *any* nucleic acid encoding a polypeptide "with at least about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a polypeptide with 50, 30 or 10 conservative amino acid substitutions".

There does not appear to be sufficient guidance in the specification as filed as to how the skilled artisan would make and use the various nucleic acids recited in the instant claims. A person of skill in the art would not know which sequences are essential, which sequences are non-essential, and what particular sequence lengths identify essential sequences. There is insufficient guidance to direct a person of skill in the art to select particular sequences or sequence lengths as essential for inhibiting the differentiation of myoblasts into myotubes . Without detailed direction as to which nucleic acid sequences are essential to the function of the encoded polypeptide, a person of skill in the art would not be able to determine without undue experimentation which of the plethora of nucleic acid sequences encompassed by the instant claims would share the ability to inhibit the differentiation of myoblasts into myotubes other than an isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1, or an isolated nucleic acid that encodes a polypeptide **consisting** of the amino acid sequence 76 through 149 of SEQ ID NO:1. Wadhwa et al., (J of Biol. Sci. 1999, 274, pages 14948 – 14955) teach that *Striamin* protein does not share any structural homology to any proteins known to be involved to any aspects of muscle differentiation and only very specific sequences of said protein are capable of repressing transcriptional activity of p53 and that characterization of the sequences essential for *Striamin* protein function has yet to be done ( see entire document, page 14954 in particular).

Furthermore, the specification fails to teach what deletions, truncations, substitutions and mutations of the disclosed sequence can be tolerated that will allow the protein to function as claimed. While it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with reasonable expectation of success are limited. Certain positions in the sequence are critical to the three-dimensional structure/function relationship, and these regions can tolerate only conservative substitutions or no substitutions. Residues that are directly involved in protein functions such as binding will certainly be among the most conserved (Bowie et al. Science, 247:1306-1310, 1990).

Since the nucleic acid sequence of a polynucleotide determines its protein coding properties, predictability of which changes can be tolerated in a polynucleotide's nucleic acid sequence and still retain similar functions and properties requires a knowledge of, and guidance with regard to which nucleic acids within the full-length nucleotide sequence, if any, are tolerant of modification and which are conserved or less tolerant to modification, and detailed knowledge of the ways in which the product's structure relates to its functional usefulness. Because there is no guidance in the specification as to which amino acid sequence within the full-length amino acid sequence of SEQ ID NO: 1, which encoded *Striamin* protein that after substitution, deletion or insertion will retain the same function, it is unpredictable to determine which polynucleotide comprising a polynucleotide sequence that encodes a polynucleotide sequence that has at least about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a

polypeptide with 50, 30 or 10 conservative amino acid substitutions will have similar function. Since the structure associated with functions of any polynucleotide mentioned above are not disclosed, predicting which polynucleotide that about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a polypeptide with 50, 30 or 10 conservative amino acid substitutions" having the same function as amino acid sequence of SEQ ID NO: 1 is well outside the realm of routine experimentation.

With regards to the comments that using the open-ended term "comprising" to permit exactly the expansion of the scope of nucleic acid claims is perfectly acceptable.

Contrary to applicant's assertion the issue raised in the previous Office Action was not about acceptability of using an open-ended term "comprising". As has been stated previously, said term expand an isolated nucleic acid molecule to include additional non disclosed nucleic acids sequences outside of the specified sequences. It means that a peptide may include additional unrecited amino acid on either or both of the N or C-terminus of a given sequence. The disclosure of polypeptide of SEQ ID NO:1, encoded by an nucleic acid consisting of nucleotides 294 through 740 of SEQ ID NO:2, wherein said polypeptide inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 cannot support the entire genus of: *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45 as part of their sequence. Applicant is relying upon certain biological activities and the disclosure of a single species to support an entire genus. As has been discussed supra, minor structural differences among even structurally related compounds or compositions can result in substantially different biology, expression, and pharmacology of proteins. Therefore, structurally unrelated *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45 as part of their sequence encompassed by the claimed invention would be expected to have greater differences in their activities.

Since the instant fact pattern fails to indicate that representative number of structurally related compounds is disclosed, the artisan would not know the identity of a reasonable number of representative compounds falling within the scope of the instant claims and consequently would not know how to make them. An assay for *finding* a product is not equivalent to a positive recitation of *how to make* a product.

Thus, Applicant has not provided sufficient guidance to enable one skill in the art to make and use claimed (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes, as claimed in claim 11, or (ii) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (iii) *any* isolated nucleic acid encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (iv) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims 37-39; or (v) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (vi) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (vii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claim 45 in a manner reasonably correlated with the scope of the claims. The scope of the claims must bear a reasonable correlation with the scope of enablement. *In re Fisher*, 166 USPQ 18 (CCPA 1970) indicates that the more unpredictable an area is, the more specific enablement is necessary in order to satisfy the statute.

In view of the quantity of experimentation necessary, the unpredictability of the art, the lack of sufficient guidance in the specification, the limited working examples, and the limited amount of direction provided given the breadth of the claims, it would take undue trials and errors to practice the claimed invention.

The following new grounds of rejection is necessitated by the amendment filed 01/06/06

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 37(c) of this title before the invention thereof by the applicant for patent.

6. Claims 47 and 48 are rejected under 35 U.S.C. 102(e) as being anticipated by US Patent 6,458,533 as is evidenced by Sambrook et al ( Molecular Cloning, 1989, Cold Spring Harbor, pages 11.2-11.7).

US Patent '533 teach an isolated 60 mer nucleic acid comprising 17 nucleotides ( SEQ ID NO:95) that are 100% identical to nucleotides 541-557 of SEQ ID NO:2.

As is evidenced by Sambrook et al., an isolated nucleic acid comprising at least 17 consecutive nucleotides that are 100 % complement to the second nucleic acid sequence would hybridizes to it under high stringency conditions . Since the office does not have a laboratory to test the reference isolated nucleic acid molecule it is applicant's burden to show that the reference nucleic acid molecule does not hybridizes to a single stranded probe as recited in the claims. See *In re Best*, 195 USPQ 430, 433 (CCPA 1977); *In re Marosi*, 218 USPQ 289, 292-293 (Fed. Cir. 1983); *In re Fitzgerald et al.*, 205 USPQ 594 (CCPA 1980).

7. Claim 13 is objected to as being dependent upon a rejected base claim 11, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

8. The prior art does not teach or suggest the claim invention recited in claims 8-10, 13, 17-19, 22-24, 28, 44, 46, 49 and 50.

9. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

10. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michail Belyavskyi whose telephone number is 571/ 272-0840 The examiner can normally be reached Monday through Friday from 9:00 AM to 5:30 PM. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on 571/ 272-0841 .

The fax number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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